RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/071,751A_
Source: _1 Fwib_
Date Processed by STIC: _10/18/05_

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: _/0/071, 751A_   CRF Edit Date: _/0/19/05_
                                                 Edited by: _Av_

____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

____ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

✓ Deleted: ✓ invalid beginning/end-of-file text ; ____ page numbers

____ Inserted mandatory headings/numeric identifiers, specifically:

_____

____ Moved responses to same line as heading/numeric identifier, specifically:

_____

____ Other:

_____
_____
_____

RAW SEQUENCE LISTING   DATE: 10/19/2005
PATENT APPLICATION: **US/10/071,751A**   TIME: 08:40:52

Input Set : **N:\AMC\071751.txt**
Output Set: **N:\CRF4\10192005\J071751A.raw**

SEQUENCE LISTING

```
 3  (1) GENERAL INFORMATION:
 5      (i) APPLICANT: Frank, Glenn R.
 6                    Wu Hunter, Shirley
 7                    Wallenfels, Lynda
 9     (ii) TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND
10                              APPARATUS TO COLLECT SUCH PROTEINS
12    (iii) NUMBER OF SEQUENCES: 88
14     (iv) CORRESPONDENCE ADDRESS:
15          (A) ADDRESSEE: SHERIDAN ROSS P.C.
16          (B) STREET: 1700 LINCOLN ST., SUITE 3500
17          (C) CITY: DENVER
18          (D) STATE: CO
19          (E) COUNTRY: U.S.A.
20          (F) ZIP: 80203
22      (v) COMPUTER READABLE FORM:
23          (A) MEDIUM TYPE: Floppy disk
24          (B) COMPUTER: IBM PC compatible
25          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28     (vi) CURRENT APPLICATION DATA:
```
C--> 29   **(A) APPLICATION NUMBER: US/10/071,751A**
C--> 30   **(B) FILING DATE: 07-Feb-2002**
```
31          (C) CLASSIFICATION:
33   (viii) ATTORNEY/AGENT INFORMATION:
34          (A) NAME: Connell, Gary J.
35          (B) REGISTRATION NUMBER: 32,020
36          (C) REFERENCE/DOCKET NUMBER: 2618-17-C4
38     (ix) TELECOMMUNICATION INFORMATION:
39          (A) TELEPHONE: 303/863-9700
40          (B) TELEFAX: 303/863-0223
46  (2) INFORMATION FOR SEQ ID NO: 1:
48      (i) SEQUENCE CHARACTERISTICS:
49          (A) LENGTH: 26 amino acids
50          (B) TYPE: amino acid
51          (C) STRANDEDNESS:
52          (D) TOPOLOGY: linear
54     (ii) MOLECULE TYPE: protein
56     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
58          Met Arg Gly Asn His Val Phe Leu Glu Asp Gly Met Ala Asp Met Thr
59          1               5                   10                  15
61          Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr
62                      20                  25
```

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          RAW SEQUENCE LISTING              DATE: 10/19/2005
          PATENT APPLICATION: US/10/071,751A    TIME: 08:40:52

          Input Set : N:\AMC\071751.txt
          Output Set: N:\CRF4\10192005\J071751A.raw

   66 (2) INFORMATION FOR SEQ ID NO: 2:
   68       (i) SEQUENCE CHARACTERISTICS:
   69           (A) LENGTH: 12 amino acids
   70           (B) TYPE: amino acid
   71           (C) STRANDEDNESS:
   72           (D) TOPOLOGY: linear
   74      (ii) MOLECULE TYPE: protein
   76      (ix) FEATURE:
   77           (A) NAME/KEY: Xaa = Tyr or Asp
   78           (B) LOCATION: 5
   80      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
W--> 82           Lys Tyr Arg Asn Xaa Xaa Thr Asn Asp Pro Gln Tyr
   83               1           5                   10
   86 (2) INFORMATION FOR SEQ ID NO: 3:
   88       (i) SEQUENCE CHARACTERISTICS:
   89           (A) LENGTH: 27 amino acids
   90           (B) TYPE: amino acid
   91           (C) STRANDEDNESS:
   92           (D) TOPOLOGY: linear
   94      (ii) MOLECULE TYPE: protein
   96      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
   98           Glu Ile Lys Arg Asn Asp Arg Glu Pro Gly Asn Leu Ser Lys Ile Arg
   99               1           5                   10                  15
  101           Thr Val Met Asp Lys Val Ile Lys Gln Thr Gln
  102                       20                  25
  110 (2) INFORMATION FOR SEQ ID NO: 4:
  112       (i) SEQUENCE CHARACTERISTICS:
  113           (A) LENGTH: 23 amino acids
  114           (B) TYPE: amino acid
  115           (C) STRANDEDNESS:
  116           (D) TOPOLOGY: linear
  118      (ii) MOLECULE TYPE: protein
  120      (ix) FEATURE:
  121           (A) NAME/KEY: Xaa = Ala or His
  122           (B) LOCATION: 8
  124      (ix) FEATURE:
  125           (A) NAME/KEY: Xaa = Ala or His
  126           (B) LOCATION: 9
  129      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
W--> 131           Leu Lys Asp Asn Asp Ile Tyr Xaa Xaa Arg Asp Ile Asn Glu Ile Leu
  132               1           5                   10                  15
  134           Arg Val Leu Asp Pro Ser Lys
  135                       20
  138 (2) INFORMATION FOR SEQ ID NO: 5:
  140       (i) SEQUENCE CHARACTERISTICS:
  141           (A) LENGTH: 27 amino acids
  142           (B) TYPE: amino acid
  143           (C) STRANDEDNESS:
  144           (D) TOPOLOGY: linear
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```
    146     (ii) MOLECULE TYPE: protein
    148     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
W--> 150          Asn Tyr Gly Arg Val Gln Ile Glu Asp Tyr Thr Xaa Ser Asn His Lys
    151          1           5                   10              15
    153          Asp Xaa Glu Glu Lys Asp Gln Ile Asn Gly Leu
    154                      20                  25
    157 (2) INFORMATION FOR SEQ ID NO: 6:
    159     (i) SEQUENCE CHARACTERISTICS:
    160          (A) LENGTH: 18 amino acids
    161          (B) TYPE: amino acid
    162          (C) STRANDEDNESS:
    163          (D) TOPOLOGY: linear
    165     (ii) MOLECULE TYPE: protein
    167     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
W--> 169          Lys Tyr Arg Asn Xaa Tyr Thr Asn Asp Pro Gln Leu Lys Leu Leu Asp
    170          1           5                   10              15
    172          Glu Gly
    175 (2) INFORMATION FOR SEQ ID NO: 7:
    177     (i) SEQUENCE CHARACTERISTICS:
    178          (A) LENGTH: 22 amino acids
    179          (B) TYPE: amino acid
    180          (C) STRANDEDNESS:
    181          (D) TOPOLOGY: linear
    183     (ii) MOLECULE TYPE: protein
    185     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
W--> 187          Tyr Phe Asn Asp Gln Ile Lys Ser Val Met Glu Pro Xaa Val Phe Lys
    188          1           5                   10              15
    190          Tyr Pro Xaa Ala Xaa Leu
    191                      20
    194 (2) INFORMATION FOR SEQ ID NO: 8:
    196     (i) SEQUENCE CHARACTERISTICS:
    197          (A) LENGTH: 20 base pairs
    198          (B) TYPE: nucleic acid
    199          (C) STRANDEDNESS: single
    200          (D) TOPOLOGY: linear
    202     (ii) MOLECULE TYPE: DNA (genomic)
    204     (ix) FEATURE:
    205          (A) NAME/KEY: misc_feature
    206          (B) LOCATION: 1..20
    207          (D) OTHER INFORMATION: /label= primer
    209     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
    211     TGRTTTCCWA TRAARTCTTC                                        20
    214 (2) INFORMATION FOR SEQ ID NO: 9:
    216     (i) SEQUENCE CHARACTERISTICS:
    217          (A) LENGTH: 225 base pairs
    218          (B) TYPE: nucleic acid
    219          (C) STRANDEDNESS: single
    220          (D) TOPOLOGY: linear
    222     (ii) MOLECULE TYPE: DNA (genomic)
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RAW SEQUENCE LISTING   DATE: 10/19/2005
PATENT APPLICATION: US/10/071,751A   TIME: 08:40:52

            Input Set : N:\AMC\071751.txt
            Output Set: N:\CRF4\10192005\J071751A.raw

224   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
226   GAATTCGGCA CGAGTGAAAT TCAATATTTT GTTTTACATT AAATTTTTCA AATTCGATAT   60
228   GAAATTTTTA CTGGCAATTT GCGTGTTGTG TGTTTTATTA AATCAAGTAT CTATGTCAAA   120
230   AATGGTCACT GAAAAGTGTA AGTCAGGTGG AAATAATCCA AGTACAGAAG AGGTGTCAAT   180
232   ACCATCTGGG AAGCTTACTA TTGAAGATTT TTGTATTGGA AATCA   225
239 (2) INFORMATION FOR SEQ ID NO: 10:
241   (i) SEQUENCE CHARACTERISTICS:
242   (A) LENGTH: 15 base pairs
243   (B) TYPE: nucleic acid
244   (C) STRANDEDNESS: single
245   (D) TOPOLOGY: linear
247   (ii) MOLECULE TYPE: DNA (genomic)
249   (ix) FEATURE:
250   (A) NAME/KEY: misc_feature
251   (B) LOCATION: 1..15
252   (D) OTHER INFORMATION: /label= primer
254   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
256   AATTCGGCAC GAGTG   15
259 (2) INFORMATION FOR SEQ ID NO: 11:
261   (i) SEQUENCE CHARACTERISTICS:
262   (A) LENGTH: 565 base pairs
263   (B) TYPE: nucleic acid
264   (C) STRANDEDNESS: single
265   (D) TOPOLOGY: linear
267   (ii) MOLECULE TYPE: cDNA
269   (ix) FEATURE:
270   (A) NAME/KEY: CDS
271   (B) LOCATION: 45..314
274   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
276   TGAAATTCAA TATTTTGTTT TACATTAAAT TTTTCAAATT CGAT ATG AAA TTT TTA   56
277   Met Lys Phe Leu
278   1
280   CTG GCA ATT TGC GTG TTG TGT GTT TTA TTA AAT CAA GTA TCT ATG TCA   104
281   Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln Val Ser Met Ser
282   5   10   15   20
284   AAA ATG GTC ACT GAA AAG TGT AAG TCA GGT GGA AAT AAT CCA AGT ACA   152
285   Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn Asn Pro Ser Thr
286   25   30   35
288   GAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT GAA GAT TTT TGT   200
289   Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile Glu Asp Phe Cys
290   40   45   50
292   ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TAC AAA AGT CAA TGT GGA   248
293   Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys Ser Gln Cys Gly
294   55   60   65
296   TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA CGA CCA AAT CAA   296
297   Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr Arg Pro Asn Gln
298   70   75   80
300   AAA CAC TGT TAT TGC GAA TAACCATATT CCGGATGAAA GACCAAATTG   344
301   Lys His Cys Tyr Cys Glu

302	85				90		
304	ATATAAATTA	CTAAAATTAT	GCTAGATAGC	AATCATAAAA	TTTTGAAGTT	TTCAATGATC	404
306	CTAACATGTT	TTGCCTCCAA	TTTATTTTAA	CAGCAAATTG	CTGGAACTTA	CCGTACCGTA	464
308	ACTAAATGTT	CAAGAAATAC	TGAATGTTTA	CAAATAGATT	ATTATAAATA	TTGTAACATT	524
310	GTCTAATATT	TATAAGAATT	ATATAAACTG	AATTGCAAAA	A		565

```
313  (2) INFORMATION FOR SEQ ID NO: 12:
315      (i) SEQUENCE CHARACTERISTICS:
316          (A) LENGTH: 90 amino acids
317          (B) TYPE: amino acid
318          (D) TOPOLOGY: linear
320      (ii) MOLECULE TYPE: protein
322      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
324      Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln
325       1               5              10                  15
327      Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn
328                      20              25                  30
330      Asn Pro Ser Thr Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile
331                  35              40                  45
333      Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys
334              50              55                  60
336      Ser Gln Cys Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr
337       65                  70                  75                  80
339      Arg Pro Asn Gln Lys His Cys Tyr Cys Glu
340                      85                  90

343  (2) INFORMATION FOR SEQ ID NO: 13:
345      (i) SEQUENCE CHARACTERISTICS:
346          (A) LENGTH: 270 base pairs
347          (B) TYPE: nucleic acid
348          (C) STRANDEDNESS: single
349          (D) TOPOLOGY: linear
351      (ii) MOLECULE TYPE: cDNA
353      (ix) FEATURE:
354          (A) NAME/KEY: CDS
355          (B) LOCATION: 1..270
358      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
360      ATG AAA TTT TTA CTG GCA ATT TGC GTG TTG TGT GTT TTA TTA AAT CAA      48
361      Met Lys Phe Leu Leu Ala Ile Cys Val Leu Cys Val Leu Leu Asn Gln
362       1               5              10                  15
364      GTA TCT ATG TCA AAA ATG GTC ACT GAA AAG TGT AAG TCA GGT GGA AAT      96
365      Val Ser Met Ser Lys Met Val Thr Glu Lys Cys Lys Ser Gly Gly Asn
366                      20              25                  30
368      AAT CCA AGT ACA GAA GAG GTG TCA ATA CCA TCT GGG AAG CTT ACT ATT     144
369      Asn Pro Ser Thr Glu Glu Val Ser Ile Pro Ser Gly Lys Leu Thr Ile
370                  35              40                  45
372      GAA GAT TTT TGT ATT GGA AAT CAT CAA AGT TGC AAA ATA TTT TAC AAA     192
373      Glu Asp Phe Cys Ile Gly Asn His Gln Ser Cys Lys Ile Phe Tyr Lys
374              50              55                  60
376      AGT CAA TGT GGA TTT GGA GGT GGT GCT TGT GGA AAC GGT GGT TCA ACA     240
377      Ser Gln Cys Gly Phe Gly Gly Gly Ala Cys Gly Asn Gly Gly Ser Thr
```

Raw Sequence Listing before editing
(for reference only)

IFW16

RAW SEQUENCE LISTING   DATE: 10/18/2005
PATENT APPLICATION: US/10/071,751A   TIME: 11:11:45

Input Set : E:\2618-17-C4-PUS-2.txt
Output Set: N:\CRF4\10182005\J071751A.raw

                    SEQUENCE LISTING
W--> 3 The following Sequence Listing is submitted pursuant to
E--> 5 submitted herewith.
E--> 7 Applicants assert pursuant to 37 CFR 1.821(f) that the
E--> 8 content of the paper and computer readable copies of SEQ ID
E--> 9 NO:1 through SEQ ID NO:88 submitted herewith are the same.

delete

     12 (1) GENERAL INFORMATION:
     14   (i) APPLICANT: Frank, Glenn R.
     15   Wu Hunter, Shirley
     16   Wallenfels, Lynda
     18   (ii) TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND
     19   APPARATUS TO COLLECT SUCH PROTEINS
     21   (iii) NUMBER OF SEQUENCES: (88)
     23   (iv) CORRESPONDENCE ADDRESS:
     24.   (A) ADDRESSEE: SHERIDAN ROSS P.C.
     25   (B) STREET: 1700 LINCOLN ST., SUITE 3500
     26   (C) CITY: DENVER
     27   (D) STATE: CO
     28   (E) COUNTRY: U.S.A.
     29   (F) ZIP: 80203
C--> 31   (v) COMPUTER READABLE FORM:
     32   (A) MEDIUM TYPE: Floppy disk
     33   (B) COMPUTER: IBM PC compatible
     34   (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     35   (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     37   (vi) CURRENT APPLICATION DATA:
C--> 38   (A) APPLICATION NUMBER: US/10/071,751A
C--> 39   (B) FILING DATE: 07-Feb-2002
     40   (C) CLASSIFICATION:
     42   (viii) ATTORNEY/AGENT INFORMATION:
     43   (A) NAME: Connell, Gary J.
     44   (B) REGISTRATION NUMBER: 32,020
     45   (C) REFERENCE/DOCKET NUMBER: 2618-17-C4
     47   (ix) TELECOMMUNICATION INFORMATION:
     48   (A) TELEPHONE: 303/863-9700
     49   (B) TELEFAX: 303/863-0223

ERRORED SEQUENCES

Does Not Comply Corrected Diskette Needed

VERIFICATION SUMMARY   DATE: 10/18/2005
PATENT APPLICATION: **US/10/071,751A**   TIME: 11:11:46

Input Set : **E:\2618-17-C4-PUS-2.txt**
Output Set: **N:\CRF4\10182005\J071751A.raw**

L:3 M:244 W: Invalid beginning of sequence listing, Data=[The following Sequence Listing is submitted pursuant to], Duplicate Sequence Listing Title!
L:4 M:220 C: Keyword misspelled or invalid format, [(v) COMPUTER READABLE FORM:]
L:5 M:243 E: Alpha Header Field expected, Data=[submitted herewith.], General Header Line Not Processed!
L:7 M:243 E: Alpha Header Field expected, Data=[Applicants assert pursuant to 37 CFR 1.821(f) that the], General Header Line Not Processed!
L:8 M:243 E: Alpha Header Field expected, Data=[content of the paper and computer readable copies of SEQ ID], General Header Line Not Processed!
L:9 M:243 E: Alpha Header Field expected, Data=[NO:1 through SEQ ID NO:88 submitted herewith are the same.], General Header Line Not Processed!
L:38 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:39 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
M:341 Repeated in SeqNo=5
L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:196 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
M:341 Repeated in SeqNo=7
L:1634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:1152
L:1770 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:368
L:3527 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70 after pos.:0
M:341 Repeated in SeqNo=70